

Temporal and Spatial Variation of Microbial Community Structures in Oil Sand Tailing Ponds

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Introduction

The process of extracting bitumen from oil sands produces large volumes of tailings that are deposited in large settling basins to become denser mature fine tailings; ultimately aiming at reclamation of the land by establishing viable environmental systems such as wetlands or lakes.

Microorganisms enhance particulate matter sedimentation rates and the dewatering of tailings materials, releasing water for bitumen extraction. They are critical to biogeochemical elemental cycles and the degradation of toxic hydrocarbon contaminants coupled to greenhouse gas production in oil sands fine fluid tailings and influence remediation and land-reclamation efforts.

Results

Microbial community patterns were analysed using population ecology tools. A bioreactor study showed that after 300 days no significant differences existed between the microbial communities of the bioreactors and the field samples. This study suggests that bioreactor studies reflect field conditions. It also proposes a whole community succession pattern from bacterial dominance to a new assemblage predominated by archaea [1].

To reinforce these findings, a comparison between different sampling locations within the same tailings ponds was carried out and shows the degree of heterogeneity of the material; comparisons between ponds of different ages give an insight into the temporal changes in the microbial community composition during the settling of the material under field conditions.

Conclusions

These results will have implications for the stepwise development of microbial model systems for predictive management of field scale tailings basins. They will aid in the determination of times and locations within the pond where greenhouse gas (CH₄ and CO₂) production is likely to happen. This will assist in managing the ponds, as well as help remediation and land reclamation efforts.

Reference

[1] Chi Fru (2012) *Environmental Science & Technology*, in review

Manipulating uranium redox status in an alluvial aquifer: insights from electron donor amendment experiments

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Introduction

Starting in 2002, field-scale biostimulation experiments have been conducted in a uranium-contaminated, shallow alluvial aquifer located along the Colorado River in western Colorado. In parallel the naturally reduced zones in the aquifer have been examined. These experiments and observations have provided insight into the coupling of microbiological, biogeochemical, and hydrogeological processes controlling mobility of uranium in subsurface environments. Research at the U.S. Department of Energy's Integrated Field Research Challenge site (IFRC) at Rifle, Colorado, USA, initially focused on testing the concept that Fe-reducing bacteria such as *Geobacter sp.* could reduce soluble U(VI) to insoluble U(IV) during electron donor amendment (acetate) and that this could be used as a bioremediation strategy for uranium-contaminated aquifers.

Summary of Results

Initial experiments demonstrated a stimulation of microbial Fe(III) reduction *in situ* that correlated with an increase in *Geobacter sp.* within the subsurface microbial community and a decrease in soluble U(VI) concentration in the groundwater consistent with laboratory studies and the known physiological trait of *Geobacter sp.* to enzymatically reduce U(VI). After approximately 20-30 days, the dominant microbial process shifted from Fe(III) reduction to sulfate reduction and U(VI) concentrations increased. Subsequent experiments directly linked gene expression for metal reduction pathways in *Geobacter sp.* to decreases in U(VI) concentration. More recently it has been possible to sample and analyze both *in situ* proteomes and metagenomes during biostimulation, leading to a comprehensive understanding of both the metabolic potential of the biostimulated microbial community and its actively expressed metabolism.

Future Directions

Future research at the Rifle IFRC will focus on understanding the plume-scale behavior of uranium in the context of the metabolic potential of the subsurface microbial community enabled by metagenomic sequencing. Initial results show assembly of nearly complete genomes for microbes present at $\geq 0.5\%$ abundance is achievable. Coupled with proteomics, transcriptomics, and selected physiological studies, prediction of microbially-mediated uranium fate and transport should be possible for aquifers under conditions that include natural microbially-mediated reduction of uranium.